

Interference - EAST

| Ref # | Hits | Search Query | DBs | Default Operator | Plurals | Time Stamp |
|-------|------|---------------------|---|------------------|---------|------------------|
| S1 | 2 | "2002156262".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:18 |
| S2 | 2 | "20020156262".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:18 |
| S3 | 5 | "2004043465".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:18 |
| S4 | 2 | "20040043465".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:19 |
| S5 | 1 | "20040082049".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:20 |
| S6 | 2 | "20040086996".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/11/08 12:08 |
| S7 | 2 | "200037655".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:21 |
| S8 | 2 | "200037655".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:22 |
| S9 | 28 | leung.in. and lpaat | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:24 |
| S10 | 2 | "2000175684".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:28 |
| S11 | 2 | "20020156262".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:53 |
| S12 | 2 | "20030073174".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2004/11/03 14:53 |

| | | | | | | |
|-----|------|---|---|----|-----|------------------|
| S13 | 2 | "6300487".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/11/08 12:07 |
| S14 | 2 | "6670143".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/06/28 16:01 |
| S15 | 2 | "6670143".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/11/08 12:05 |
| S16 | 2 | "6136964".pn. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/11/08 12:07 |
| S17 | 5003 | leung.in. or adourel.in. or hollenback. in. | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/11/08 12:09 |
| S18 | 9 | S17 and (lysophosphatidic and (SEQ adj ID).clm.) | US-PGPUB; USPAT; EPO; JPO; DERWENT | OR | OFF | 2005/11/08 12:09 |

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 17:58:26 ; Search time 3812 Seconds
(without alignments)
3991.327 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140055_12066/app_query.fasta_1.455

-DB=GenEmbl -QFMT=fastap -SUFFIX=na.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462_@CGN_1_1_5600_@runat_14062005_140055_12066 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*

12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|------------------|--------|----|----------|--------------------|
| 1 | 1682 | 100.0 | 1314 | 6 | CQ731857 | CQ731857 Sequence |
| 2 | 1682 | 100.0 | 1333 | 6 | E39269 | E39269 Gene encodi |
| 3 | 1682 | 100.0 | 1333 | 9 | AB040138 | AB040138 Homo sapi |
| 4 | 1682 | 100.0 | 1523 | 6 | BD265489 | BD265489 Mammalian |
| 5 | 1682 | 100.0 | 1523 | 6 | AR370495 | AR370495 Sequence |
| 6 | 1682 | 100.0 | 1523 | 6 | AR442694 | AR442694 Sequence |
| 7 | 1682 | 100.0 | 1523 | 9 | AF156775 | AF156775 Homo sapi |
| 8 | 1682 | 100.0 | 1577 | 9 | BC011971 | BC011971 Homo sapi |
| 9 | 1682 | 100.0 | 1660 | 6 | BD265488 | BD265488 Mammalian |
| 10 | 1682 | 100.0 | 1660 | 6 | AR370494 | AR370494 Sequence |
| 11 | 1682 | 100.0 | 1660 | 6 | AR442693 | AR442693 Sequence |
| 12 | 1682 | 100.0 | 1660 | 9 | AF156774 | AF156774 Homo sapi |
| 13 | 1682 | 100.0 | 1960 | 6 | AX317982 | AX317982 Sequence |
| 14 | 1682 | 100.0 | 2377 | 9 | BC063552 | BC063552 Homo sapi |
| 15 | 1682 | 100.0 | 2397 | 9 | BC040603 | BC040603 Homo sapi |
| 16 | 1678 | 99.8 | 1128 | 6 | AX239832 | AX239832 Sequence |
| 17 | 1678 | 99.8 | 1832 | 6 | AX239824 | AX239824 Sequence |
| 18 | 1662 | 98.8 | 3955 | 6 | CQ842883 | CQ842883 Sequence |
| 19 | 1662 | 98.8 | 3955 | 9 | AK125804 | AK125804 Homo sapi |
| 20 | 1598 | 95.0 | 1153 | 10 | AY167588 | AY167588 Mus muscu |
| 21 | 1598 | 95.0 | 3378 | 10 | BC058519 | BC058519 Mus muscu |
| 22 | 1598 | 95.0 | 3379 | 10 | BC052382 | BC052382 Mus muscu |
| 23 | 1593.5 | 94.7 | 3060 | 6 | AX376270 | AX376270 Sequence |
| 24 | 1593.5 | 94.7 | 3060 | 6 | AX697228 | AX697228 Sequence |
| 25 | 1593.5 | 94.7 | 3060 | 9 | AY358704 | AY358704 Homo sapi |
| 26 | 1561 | 92.8 | 5633 | 6 | BD183432 | BD183432 Novel gen |
| 27 | 1538 | 91.4 | 1769 | 6 | AR339350 | AR339350 Sequence |
| 28 | 1432 | 85.1 | 4208 | 5 | BC081052 | BC081052 Xenopus l |
| 29 | 1428 | 84.9 | 2728 | 5 | BC081323 | BC081323 Xenopus t |
| 30 | 1420 | 84.4 | 3509 | 5 | BC043776 | BC043776 Xenopus l |
| 31 | 1387 | 82.5 | 3878 | 6 | AX211367 | AX211367 Sequence |
| 32 | 1286.5 | 76.5 | 2447 | 5 | BC049474 | BC049474 Danio rer |
| 33 | 1145 | 68.1 | 1245 | 5 | BX929790 | BX929790 Gallus ga |
| 34 | 1138 | 67.7 | 1540 | 5 | BC071000 | BC071000 Xenopus l |
| 35 | 1094 | 65.0 | 1137 | 6 | AX119047 | AX119047 Sequence |
| 36 | 1094 | 65.0 | 1721 | 9 | BC020209 | BC020209 Homo sapi |
| 37 | 1094 | 65.0 | 1771 | 6 | AX135548 | AX135548 Sequence |
| 38 | 1094 | 65.0 | 1774 | 6 | BD265490 | BD265490 Mammalian |
| 39 | 1094 | 65.0 | 1774 | 6 | AR370496 | AR370496 Sequence |
| 40 | 1094 | 65.0 | 1774 | 6 | AR442695 | AR442695 Sequence |
| 41 | 1094 | 65.0 | 1774 | 9 | AF156776 | AF156776 Homo sapi |
| 42 | 1094 | 65.0 | 1781 | 6 | AR252488 | AR252488 Sequence |
| 43 | 1094 | 65.0 | 1781 | 6 | AR528661 | AR528661 Sequence |
| 44 | 1094 | 65.0 | 1781 | 6 | AX056649 | AX056649 Sequence |

45 1094 65.0 1781 6 AX403268

AX403268 Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 17:41:30 ; Search time 517 Seconds
(without alignments)
3595.355 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140055_12057/app_query.fasta_1.455

-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=na.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462_@CGN_1_1_708_@runat_14062005_140055_12057 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|------------------|--------|----|----------|--------------------|
| 1 | 1682 | 100.0 | 1333 | 3 | AAA71493 | Aaa71493 Human lys |
| 2 | 1682 | 100.0 | 1523 | 3 | AAA51069 | Aaa51069 Human LPA |
| 3 | 1682 | 100.0 | 1523 | 6 | AAD24424 | Aad24424 Human LPA |
| 4 | 1682 | 100.0 | 1523 | 9 | ABX16125 | Abx16125 Human cDN |
| 5 | 1682 | 100.0 | 1523 | 12 | ADJ93798 | Adj93798 Human lys |
| 6 | 1682 | 100.0 | 1523 | 12 | ADN49482 | Adn49482 Human lys |
| 7 | 1682 | 100.0 | 1523 | 12 | ADO04621 | Ado04621 Human lys |
| 8 | 1682 | 100.0 | 1629 | 6 | ABL55080 | Abl55080 Human cDN |
| 9 | 1682 | 100.0 | 1646 | 12 | ADQ85949 | Adq85949 Human tum |
| 10 | 1682 | 100.0 | 1660 | 3 | AAA51068 | Aaa51068 Human LPA |
| 11 | 1682 | 100.0 | 1660 | 6 | AAD24423 | Aad24423 Human LPA |
| 12 | 1682 | 100.0 | 1660 | 9 | ABX16124 | Abx16124 Human cDN |
| 13 | 1682 | 100.0 | 1660 | 12 | ADJ93796 | Adj93796 Human lys |
| 14 | 1682 | 100.0 | 1660 | 12 | ADN49480 | Adn49480 Human lys |
| 15 | 1682 | 100.0 | 1660 | 12 | ADO04619 | Ado04619 Human lys |
| 16 | 1682 | 100.0 | 1660 | 13 | ACN40851 | Acn40851 Tumour-as |
| 17 | 1682 | 100.0 | 1960 | 6 | AAD24014 | Aad24014 Human dru |
| 18 | 1678 | 99.8 | 1832 | 5 | AAH75152 | Aah75152 Nucleotid |
| 19 | 1678 | 99.8 | 1832 | 12 | ADQ15077 | Adq15077 Human can |
| 20 | 1678 | 99.8 | 1832 | 13 | ADR40140 | Adr40140 Human lys |
| 21 | 1662 | 98.8 | 3955 | 12 | ADQ64369 | Adq64369 Novel hum |
| 22 | 1593.5 | 94.7 | 3059 | 4 | AAS46093 | Aas46093 Human DNA |
| 23 | 1593.5 | 94.7 | 3060 | 3 | AAA37104 | Aaa37104 Human PRO |
| 24 | 1593.5 | 94.7 | 3060 | 4 | AAF54413 | Aaf54413 Primer #8 |
| 25 | 1593.5 | 94.7 | 3060 | 8 | ACA89543 | Aca89543 cDNA enco |
| 26 | 1593.5 | 94.7 | 3060 | 8 | ACA73553 | Aca73553 Human sec |
| 27 | 1593.5 | 94.7 | 3060 | 8 | ACA05868 | Aca05868 Human sec |
| 28 | 1593.5 | 94.7 | 3060 | 8 | ACA66702 | Aca66702 cDNA enco |
| 29 | 1593.5 | 94.7 | 3060 | 8 | ACF20277 | Acf20277 Human sec |
| 30 | 1593.5 | 94.7 | 3060 | 8 | ACF19663 | Acf19663 Human sec |
| 31 | 1593.5 | 94.7 | 3060 | 8 | ACD21951 | Acd21951 Human sec |
| 32 | 1593.5 | 94.7 | 3060 | 8 | ACF13116 | Acf13116 Human sec |
| 33 | 1593.5 | 94.7 | 3060 | 8 | ACD25219 | Acd25219 Human sec |
| 34 | 1593.5 | 94.7 | 3060 | 8 | ACF00268 | Acf00268 Human sec |
| 35 | 1593.5 | 94.7 | 3060 | 8 | ACA72325 | Aca72325 Novel hum |
| 36 | 1593.5 | 94.7 | 3060 | 8 | ACD04849 | Acd04849 Novel hum |
| 37 | 1593.5 | 94.7 | 3060 | 8 | ACD18310 | Acd18310 Human sec |
| 38 | 1593.5 | 94.7 | 3060 | 8 | ACD08317 | Acd08317 Human sec |
| 39 | 1593.5 | 94.7 | 3060 | 8 | ACA88751 | Aca88751 Novel hum |
| 40 | 1593.5 | 94.7 | 3060 | 8 | ACA70193 | Aca70193 Human sec |
| 41 | 1593.5 | 94.7 | 3060 | 8 | ACD12415 | Acd12415 Novel hum |
| 42 | 1593.5 | 94.7 | 3060 | 8 | ACC74330 | Acc74330 Human sec |
| 43 | 1593.5 | 94.7 | 3060 | 8 | ACD15958 | Acd15958 Human sec |
| 44 | 1593.5 | 94.7 | 3060 | 8 | ACD25526 | Acd25526 Novel hum |
| 45 | 1593.5 | 94.7 | 3060 | 8 | ACD18003 | Acd18003 Human sec |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 18:06:16 ; Search time 188 Seconds
(without alignments)
2732.930 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140056_12095/app_query.fasta_1
.455

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=na.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462 @CGN_1_1_105 @runat_14062005_140056_12095 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | | | Description |
|--------|-----|-------|-------------|--------|----|----------------------|-------------------|
| | No. | Score | Query Match | Length | DB | ID | |
| | 1 | 1682 | 100.0 | 1523 | 3 | US-09-215-252-14 | Sequence 14, Appl |
| | 2 | 1682 | 100.0 | 1523 | 4 | US-09-970-989A-14 | Sequence 14, Appl |
| | 3 | 1682 | 100.0 | 1660 | 3 | US-09-215-252-12 | Sequence 12, Appl |
| | 4 | 1682 | 100.0 | 1660 | 4 | US-09-970-989A-12 | Sequence 12, Appl |
| | 5 | 1538 | 91.4 | 1769 | 4 | US-09-620-312D-841 | Sequence 841, App |
| | 6 | 1094 | 65.0 | 1774 | 3 | US-09-215-252-16 | Sequence 16, Appl |
| | 7 | 1094 | 65.0 | 1774 | 4 | US-09-970-989A-16 | Sequence 16, Appl |
| | 8 | 513 | 30.5 | 1515 | 4 | US-08-818-581B-3 | Sequence 3, Appli |
| | 9 | 496.5 | 29.5 | 1514 | 2 | US-08-454-267-1 | Sequence 1, Appli |
| | 10 | 496.5 | 29.5 | 1514 | 2 | US-08-941-319-1 | Sequence 1, Appli |
| | 11 | 496.5 | 29.5 | 1514 | 3 | US-09-035-098-1 | Sequence 1, Appli |
| | 12 | 247 | 14.7 | 271 | 4 | US-09-513-999C-10074 | Sequence 10074, A |
| | 13 | 231 | 13.7 | 1763 | 4 | US-09-620-312D-637 | Sequence 637, App |
| | 14 | 228 | 13.6 | 5227 | 2 | US-08-996-306-3 | Sequence 3, Appli |
| | 15 | 228 | 13.6 | 5245 | 3 | US-09-338-907-3 | Sequence 3, Appli |
| | 16 | 228 | 13.6 | 5245 | 3 | US-09-218-207-3 | Sequence 3, Appli |
| | 17 | 228 | 13.6 | 5290 | 3 | US-09-338-907-119 | Sequence 119, App |
| | 18 | 228 | 13.6 | 5290 | 3 | US-09-218-207-119 | Sequence 119, App |
| | 19 | 222 | 13.2 | 5250 | 3 | US-09-338-907-69 | Sequence 69, Appl |
| | 20 | 222 | 13.2 | 5250 | 3 | US-09-218-207-69 | Sequence 69, Appl |
| | 21 | 219.5 | 13.0 | 1409 | 3 | US-09-338-907-72 | Sequence 72, Appl |
| | 22 | 219.5 | 13.0 | 1409 | 3 | US-09-338-907-184 | Sequence 184, App |
| | 23 | 219.5 | 13.0 | 1409 | 3 | US-09-218-207-72 | Sequence 72, Appl |
| | 24 | 219.5 | 13.0 | 1409 | 3 | US-09-218-207-184 | Sequence 184, App |
| | 25 | 195.5 | 11.6 | 5148 | 3 | US-09-338-907-112 | Sequence 112, App |
| | 26 | 195.5 | 11.6 | 5148 | 3 | US-09-218-207-112 | Sequence 112, App |
| | 27 | 191.5 | 11.4 | 5326 | 3 | US-09-338-907-124 | Sequence 124, App |
| | 28 | 191.5 | 11.4 | 5326 | 3 | US-09-218-207-124 | Sequence 124, App |
| | 29 | 186 | 11.1 | 5234 | 3 | US-09-338-907-113 | Sequence 113, App |
| | 30 | 186 | 11.1 | 5234 | 3 | US-09-218-207-113 | Sequence 113, App |
| | 31 | 177 | 10.5 | 5044 | 3 | US-09-338-907-115 | Sequence 115, App |
| | 32 | 177 | 10.5 | 5044 | 3 | US-09-218-207-115 | Sequence 115, App |
| | 33 | 174.5 | 10.4 | 4958 | 3 | US-09-338-907-116 | Sequence 116, App |
| | 34 | 174.5 | 10.4 | 4958 | 3 | US-09-218-207-116 | Sequence 116, App |
| | 35 | 173 | 10.3 | 775 | 4 | US-09-220-132-191 | Sequence 191, App |
| | 36 | 170 | 10.1 | 5020 | 3 | US-09-338-907-120 | Sequence 120, App |
| | 37 | 170 | 10.1 | 5020 | 3 | US-09-218-207-120 | Sequence 120, App |
| c | 38 | 165 | 9.8 | 1629 | 4 | US-09-252-991A-13111 | Sequence 13111, A |
| | 39 | 161.5 | 9.6 | 960 | 4 | US-09-540-236-1906 | Sequence 1906, Ap |
| c | 40 | 161.5 | 9.6 | 31940 | 4 | US-09-596-002-13 | Sequence 13, Appl |
| | 41 | 161 | 9.6 | 969 | 4 | US-09-252-991A-12688 | Sequence 12688, A |
| | 42 | 161 | 9.6 | 1041 | 4 | US-09-252-991A-12831 | Sequence 12831, A |
| | 43 | 152 | 9.0 | 1095 | 4 | US-09-252-991A-5981 | Sequence 5981, Ap |
| | 44 | 152 | 9.0 | 1200 | 4 | US-09-252-991A-5964 | Sequence 5964, Ap |
| c | 45 | 152 | 9.0 | 1515 | 4 | US-09-252-991A-5909 | Sequence 5909, Ap |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 19:42:57 ; Search time 571 Seconds
(without alignments)
3408.940 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140058_12181/app_query.fasta_1.455

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=na.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10667462 @CGN_1_1_723 @runat_14062005_140058_12181
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|--------|-------|-------|--------|-------------------|----|-------------------|
| No. | Score | Query | Match | Length | DB | ID | Description |
| 1 | 1682 | 100.0 | 1523 | 9 | US-09-970-989-14 | | Sequence 14, Appl |
| 2 | 1682 | 100.0 | 1523 | 18 | US-10-667-494-14 | | Sequence 14, Appl |
| 3 | 1682 | 100.0 | 1523 | 18 | US-10-667-462-14 | | Sequence 14, Appl |
| 4 | 1682 | 100.0 | 1523 | 18 | US-10-667-464-14 | | Sequence 14, Appl |
| 5 | 1682 | 100.0 | 1660 | 9 | US-09-970-989-12 | | Sequence 12, Appl |
| 6 | 1682 | 100.0 | 1660 | 18 | US-10-667-494-12 | | Sequence 12, Appl |
| 7 | 1682 | 100.0 | 1660 | 18 | US-10-667-462-12 | | Sequence 12, Appl |
| 8 | 1682 | 100.0 | 1660 | 18 | US-10-667-464-12 | | Sequence 12, Appl |
| 9 | 1682 | 100.0 | 1960 | 17 | US-10-296-606-22 | | Sequence 22, Appl |
| 10 | 1678 | 99.8 | 1128 | 9 | US-09-798-029-13 | | Sequence 13, Appl |
| 11 | 1678 | 99.8 | 1832 | 9 | US-09-798-029-5 | | Sequence 5, Appli |
| 12 | 1678 | 99.8 | 1832 | 20 | US-10-737-450-35 | | Sequence 35, Appl |
| 13 | 1678 | 99.8 | 1832 | 21 | US-10-772-636-21 | | Sequence 21, Appl |
| 14 | 1593.5 | 94.7 | 3060 | 10 | US-09-946-374-296 | | Sequence 296, App |
| 15 | 1593.5 | 94.7 | 3060 | 13 | US-10-052-586-337 | | Sequence 337, App |
| 16 | 1593.5 | 94.7 | 3060 | 14 | US-10-174-590-337 | | Sequence 337, App |
| 17 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-758-337 | | Sequence 337, App |
| 18 | 1593.5 | 94.7 | 3060 | 14 | US-10-175-737-337 | | Sequence 337, App |
| 19 | 1593.5 | 94.7 | 3060 | 14 | US-10-174-581-337 | | Sequence 337, App |
| 20 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-483-337 | | Sequence 337, App |
| 21 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-749-337 | | Sequence 337, App |
| 22 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-914-337 | | Sequence 337, App |
| 23 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-915-337 | | Sequence 337, App |
| 24 | 1593.5 | 94.7 | 3060 | 14 | US-10-173-706-337 | | Sequence 337, App |
| 25 | 1593.5 | 94.7 | 3060 | 14 | US-10-175-738-337 | | Sequence 337, App |
| 26 | 1593.5 | 94.7 | 3060 | 14 | US-10-175-752-337 | | Sequence 337, App |
| 27 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-482-337 | | Sequence 337, App |
| 28 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-757-337 | | Sequence 337, App |
| 29 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-913-337 | | Sequence 337, App |
| 30 | 1593.5 | 94.7 | 3060 | 14 | US-10-180-552-337 | | Sequence 337, App |
| 31 | 1593.5 | 94.7 | 3060 | 14 | US-10-180-557-337 | | Sequence 337, App |
| 32 | 1593.5 | 94.7 | 3060 | 14 | US-10-173-700-337 | | Sequence 337, App |

| | | | | | | |
|----|--------|------|------|----|-------------------|-------------------|
| 33 | 1593.5 | 94.7 | 3060 | 14 | US-10-174-572-337 | Sequence 337, App |
| 34 | 1593.5 | 94.7 | 3060 | 14 | US-10-174-579-337 | Sequence 337, App |
| 35 | 1593.5 | 94.7 | 3060 | 14 | US-10-174-582-337 | Sequence 337, App |
| 36 | 1593.5 | 94.7 | 3060 | 14 | US-10-174-588-337 | Sequence 337, App |
| 37 | 1593.5 | 94.7 | 3060 | 14 | US-10-175-739-337 | Sequence 337, App |
| 38 | 1593.5 | 94.7 | 3060 | 14 | US-10-175-740-337 | Sequence 337, App |
| 39 | 1593.5 | 94.7 | 3060 | 14 | US-10-175-743-337 | Sequence 337, App |
| 40 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-488-337 | Sequence 337, App |
| 41 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-492-337 | Sequence 337, App |
| 42 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-747-337 | Sequence 337, App |
| 43 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-750-337 | Sequence 337, App |
| 44 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-985-337 | Sequence 337, App |
| 45 | 1593.5 | 94.7 | 3060 | 14 | US-10-176-987-337 | Sequence 337, App |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2005, 18:05:07 ; Search time 3118 Seconds
(without alignments)
3833.284 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

- Q=/cgn2_1/USPTO_spool_p/US10667462/runat_14062005_140056_12079/app_query.fasta_1.455

-DB=EST -QFMT=fastap -SUFFIX=na.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10667462 @CGN_1_1_5180 @runat_14062005_140056_12079 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | % Query Match Length | DB | ID | Description |
|--------|-----|--------|----------------------------|------|----|-------------|
| | 1 | 1619 | 96.3 | 5079 | 3 | HSM804230 |
| | 2 | 1598 | 95.0 | 1319 | 3 | AK015906 |
| | 3 | 1598 | 95.0 | 1415 | 3 | AK076414 |
| | 4 | 1598 | 95.0 | 3022 | 3 | BC033444 |
| | 5 | 1598 | 95.0 | 3439 | 3 | AK075715 |
| | 6 | 1589 | 94.5 | 3240 | 3 | AK030607 |
| | 7 | 1513 | 90.0 | 1558 | 3 | AK008965 |
| c | 8 | 1415.5 | 84.2 | 986 | 4 | BI408757 |
| | 9 | 1388 | 82.5 | 1063 | 4 | BM459459 |
| | 10 | 1374 | 81.7 | 1131 | 9 | AY419544 |
| | 11 | 1303 | 77.5 | 1131 | 9 | AY419546 |
| | 12 | 1279 | 76.0 | 797 | 7 | CO886199 |
| | 13 | 1260 | 74.9 | 808 | 5 | BU126102 |
| | 14 | 1258.5 | 74.8 | 985 | 5 | BQ072125 |
| | 15 | 1245 | 74.0 | 735 | 6 | CD350550 |
| c | 16 | 1172.5 | 69.7 | 881 | 4 | BI100258 |
| | 17 | 1165.5 | 69.3 | 1183 | 6 | CD505010 |
| | 18 | 1141 | 67.8 | 1131 | 9 | AY419545 |
| c | 19 | 1138 | 67.7 | 675 | 4 | BM675712 |
| | 20 | 1137 | 67.6 | 669 | 7 | CO432267 |
| | 21 | 1120 | 66.6 | 656 | 2 | AW411232 |
| | 22 | 1113 | 66.2 | 827 | 6 | CD303142 |
| | 23 | 1105.5 | 65.7 | 1024 | 4 | BG424827 |
| | 24 | 1094 | 65.0 | 1137 | 9 | AY404676 |
| | 25 | 1094 | 65.0 | 1690 | 3 | CR609642 |
| | 26 | 1094 | 65.0 | 1737 | 3 | CR615061 |
| | 27 | 1094 | 65.0 | 1756 | 3 | CR623504 |
| | 28 | 1094 | 65.0 | 1781 | 3 | CR615644 |
| | 29 | 1094 | 65.0 | 1786 | 3 | CR612654 |
| | 30 | 1090 | 64.8 | 703 | 4 | BG995044 |
| | 31 | 1085 | 64.5 | 971 | 5 | BX401713 |
| | 32 | 1085 | 64.5 | 1912 | 3 | AK005139 |
| | 33 | 1085 | 64.5 | 2084 | 3 | BC031179 |
| | 34 | 1083 | 64.4 | 1137 | 9 | AY404678 |
| | 35 | 1080 | 64.2 | 976 | 5 | BU840364 |
| | 36 | 1071 | 63.7 | 648 | 2 | AW410448 |
| | 37 | 1070 | 63.6 | 637 | 7 | CF744159 |
| | 38 | 1070 | 63.6 | 1137 | 9 | AY404677 |
| c | 39 | 1063 | 63.2 | 871 | 7 | CK773096 |
| | 40 | 1060 | 63.0 | 780 | 5 | BU421664 |
| | 41 | 1058 | 62.9 | 622 | 2 | BE298682 |
| | 42 | 1051.5 | 62.5 | 896 | 4 | BG541849 |
| | 43 | 1048 | 62.3 | 919 | 5 | BX325280 |
| | 44 | 1045 | 62.1 | 871 | 7 | CR565259 |
| | 45 | 1035.5 | 61.6 | 1144 | 5 | BQ049014 |

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OM protein - protein search, using sw model

Run on: June 14, 2005, 16:00:31 ; Search time 119 Seconds
(without alignments)
1020.527 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFDTQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 1682 | 100.0 | 314 | 3 | AA96591 | Aay96591 Human lys |
| 2 | 1682 | 100.0 | 314 | 5 | AAE15295 | Aae15295 Human LPA |
| 3 | 1682 | 100.0 | 314 | 6 | ABG74254 | Abg74254 Human LPA |
| 4 | 1682 | 100.0 | 314 | 8 | ADJ93799 | Adj93799 Human lys |
| 5 | 1682 | 100.0 | 314 | 8 | ADN49483 | Adn49483 Human lys |
| 6 | 1682 | 100.0 | 314 | 8 | ADO04622 | Ado04622 Human lys |
| 7 | 1682 | 100.0 | 376 | 3 | AA96590 | Aay96590 Human lys |
| 8 | 1682 | 100.0 | 376 | 3 | AAB10460 | Aab10460 Human lys |
| 9 | 1682 | 100.0 | 376 | 5 | AAE15294 | Aae15294 Human LPA |
| 10 | 1682 | 100.0 | 376 | 5 | ABG64898 | Abg64898 Human alb |

| | | | | | | | | |
|----|--------|-------|-----|---|----------|----------|---------|-----|
| 11 | 1682 | 100.0 | 376 | 5 | ABB77011 | Abb77011 | Human | pro |
| 12 | 1682 | 100.0 | 376 | 5 | AAE14446 | Aae14446 | Human | dru |
| 13 | 1682 | 100.0 | 376 | 6 | ABG74253 | Abg74253 | Human | LPA |
| 14 | 1682 | 100.0 | 376 | 8 | ADL78165 | Adl78165 | Albumin | f |
| 15 | 1682 | 100.0 | 376 | 8 | ADJ93797 | Adj93797 | Human | lys |
| 16 | 1682 | 100.0 | 376 | 8 | ADN49481 | Adn49481 | Human | lys |
| 17 | 1682 | 100.0 | 376 | 8 | ADO04620 | Ado04620 | Human | lys |
| 18 | 1682 | 100.0 | 376 | 8 | ABM82301 | Abm82301 | Tumour | -as |
| 19 | 1678 | 99.8 | 376 | 4 | AAG67124 | Aag67124 | Amino | aci |
| 20 | 1678 | 99.8 | 376 | 8 | ADQ15078 | Adq15078 | Human | can |
| 21 | 1678 | 99.8 | 376 | 8 | ADR40141 | Adr40141 | Human | lys |
| 22 | 1662 | 98.8 | 392 | 8 | ADQ66557 | Adq66557 | Novel | hum |
| 23 | 1585.5 | 94.3 | 368 | 3 | AAV99422 | Aay99422 | Human | PRO |
| 24 | 1585.5 | 94.3 | 368 | 4 | AAB66171 | Aab66171 | Protein | o |
| 25 | 1585.5 | 94.3 | 368 | 4 | AAU29192 | Aau29192 | Human | PRO |
| 26 | 1585.5 | 94.3 | 368 | 6 | ABU58568 | Abu58568 | Human | PRO |
| 27 | 1585.5 | 94.3 | 368 | 6 | ABU88116 | Abu88116 | Novel | hum |
| 28 | 1585.5 | 94.3 | 368 | 6 | ABU84431 | Abu84431 | Human | sec |
| 29 | 1585.5 | 94.3 | 368 | 6 | ABR66305 | Abr66305 | Human | sec |
| 30 | 1585.5 | 94.3 | 368 | 6 | ABR65695 | Abr65695 | Human | sec |
| 31 | 1585.5 | 94.3 | 368 | 6 | ABU99635 | Abu99635 | Human | sec |
| 32 | 1585.5 | 94.3 | 368 | 6 | ABU82874 | Abu82874 | Human | PRO |
| 33 | 1585.5 | 94.3 | 368 | 6 | ABU89995 | Abu89995 | Novel | hum |
| 34 | 1585.5 | 94.3 | 368 | 6 | ABR68244 | Abr68244 | Human | sec |
| 35 | 1585.5 | 94.3 | 368 | 6 | ABU96297 | Abu96297 | Novel | hum |
| 36 | 1585.5 | 94.3 | 368 | 6 | ABU92728 | Abu92728 | Human | sec |
| 37 | 1585.5 | 94.3 | 368 | 6 | ABO08805 | Abo08805 | Human | sec |
| 38 | 1585.5 | 94.3 | 368 | 6 | ABO02857 | Abo02857 | Human | sec |
| 39 | 1585.5 | 94.3 | 368 | 6 | ABR75011 | Abr75011 | Human | sec |
| 40 | 1585.5 | 94.3 | 368 | 6 | ABR94773 | Abr94773 | Human | sec |
| 41 | 1585.5 | 94.3 | 368 | 6 | ABU85746 | Abu85746 | Human | PRO |
| 42 | 1585.5 | 94.3 | 368 | 6 | ABU98906 | Abu98906 | Novel | hum |
| 43 | 1585.5 | 94.3 | 368 | 6 | ABU98121 | Abu98121 | Novel | hum |
| 44 | 1585.5 | 94.3 | 368 | 6 | ABU91827 | Abu91827 | Novel | hum |
| 45 | 1585.5 | 94.3 | 368 | 6 | ABU89520 | Abu89520 | Human | PRO |

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OM protein - protein search, using sw model

Run on: June 14, 2005, 17:25:00 ; Search time 45 Seconds
(without alignments)
520.885 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % | | Query Match Length DB | ID | Description |
|---------------|-------|-------|--------------------------|-------------------|-------------------|
| | Score | Match | | | |
| 1 | 1682 | 100.0 | 314 3 | US-09-215-252-15 | Sequence 15, Appl |
| 2 | 1682 | 100.0 | 314 4 | US-09-970-989A-15 | Sequence 15, Appl |
| 3 | 1682 | 100.0 | 376 3 | US-09-215-252-13 | Sequence 13, Appl |
| 4 | 1682 | 100.0 | 376 4 | US-09-970-989A-13 | Sequence 13, Appl |
| 5 | 1094 | 65.0 | 378 3 | US-09-215-252-17 | Sequence 17, Appl |
| 6 | 1094 | 65.0 | 378 4 | US-09-970-989A-17 | Sequence 17, Appl |
| 7 | 513 | 30.5 | 377 4 | US-08-818-581B-4 | Sequence 4, Appli |
| 8 | 496.5 | 29.5 | 374 2 | US-08-454-267-2 | Sequence 2, Appli |
| 9 | 496.5 | 29.5 | 374 2 | US-08-454-267-6 | Sequence 6, Appli |
| 10 | 496.5 | 29.5 | 374 2 | US-08-941-319-2 | Sequence 2, Appli |
| 11 | 496.5 | 29.5 | 374 2 | US-08-941-319-6 | Sequence 6, Appli |
| 12 | 496.5 | 29.5 | 374 3 | US-09-035-098-2 | Sequence 2, Appli |

| | | | | | | |
|----|-------|------|-----|---|----------------------|-------------------|
| 13 | 496.5 | 29.5 | 374 | 3 | US-09-035-098-6 | Sequence 6, Appli |
| 14 | 496.5 | 29.5 | 374 | 3 | US-09-215-252-5 | Sequence 5, Appli |
| 15 | 496.5 | 29.5 | 374 | 4 | US-09-970-989A-5 | Sequence 5, Appli |
| 16 | 488.5 | 29.0 | 375 | 4 | US-08-818-581B-5 | Sequence 5, Appli |
| 17 | 389.5 | 23.2 | 295 | 2 | US-08-454-267-7 | Sequence 7, Appli |
| 18 | 389.5 | 23.2 | 295 | 2 | US-08-941-319-7 | Sequence 7, Appli |
| 19 | 389.5 | 23.2 | 295 | 3 | US-09-035-098-7 | Sequence 7, Appli |
| 20 | 389.5 | 23.2 | 311 | 4 | US-08-818-581B-6 | Sequence 6, Appli |
| 21 | 228 | 13.6 | 353 | 2 | US-08-996-306-4 | Sequence 4, Appli |
| 22 | 228 | 13.6 | 353 | 3 | US-09-338-907-4 | Sequence 4, Appli |
| 23 | 228 | 13.6 | 353 | 3 | US-09-218-207-4 | Sequence 4, Appli |
| 24 | 228 | 13.6 | 364 | 2 | US-08-996-306-5 | Sequence 5, Appli |
| 25 | 228 | 13.6 | 364 | 3 | US-09-338-907-5 | Sequence 5, Appli |
| 26 | 228 | 13.6 | 364 | 3 | US-09-218-207-5 | Sequence 5, Appli |
| 27 | 219.5 | 13.0 | 354 | 3 | US-09-338-907-74 | Sequence 74, Appl |
| 28 | 219.5 | 13.0 | 354 | 3 | US-09-218-207-74 | Sequence 74, Appl |
| 29 | 177 | 10.5 | 291 | 3 | US-09-338-907-127 | Sequence 127, App |
| 30 | 177 | 10.5 | 291 | 3 | US-09-218-207-127 | Sequence 127, App |
| 31 | 175.5 | 10.4 | 228 | 3 | US-09-338-907-70 | Sequence 70, Appl |
| 32 | 175.5 | 10.4 | 228 | 3 | US-09-218-207-70 | Sequence 70, Appl |
| 33 | 174.5 | 10.4 | 261 | 3 | US-09-338-907-128 | Sequence 128, App |
| 34 | 174.5 | 10.4 | 261 | 3 | US-09-218-207-128 | Sequence 128, App |
| 35 | 161.5 | 9.6 | 319 | 4 | US-09-540-236-3826 | Sequence 3826, Ap |
| 36 | 161 | 9.6 | 346 | 4 | US-09-252-991A-29402 | Sequence 29402, A |
| 37 | 152 | 9.0 | 364 | 4 | US-09-252-991A-22552 | Sequence 22552, A |
| 38 | 148.5 | 8.8 | 321 | 4 | US-09-328-352-5730 | Sequence 5730, Ap |
| 39 | 135 | 8.0 | 320 | 4 | US-09-489-039A-10418 | Sequence 10418, A |
| 40 | 133 | 7.9 | 23 | 3 | US-09-215-252-29 | Sequence 29, Appl |
| 41 | 133 | 7.9 | 23 | 4 | US-09-970-989A-29 | Sequence 29, Appl |
| 42 | 130 | 7.7 | 315 | 3 | US-09-338-907-134 | Sequence 134, App |
| 43 | 130 | 7.7 | 315 | 3 | US-09-218-207-134 | Sequence 134, App |
| 44 | 122.5 | 7.3 | 300 | 3 | US-09-338-907-135 | Sequence 135, App |
| 45 | 122.5 | 7.3 | 300 | 3 | US-09-218-207-135 | Sequence 135, App |

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OM protein - protein search, using sw model

Run on: June 14, 2005, 17:39:11 ; Search time 1394 Seconds
(without alignments)
86.346 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|--------|-------------|--------|----|--------------------|-------------------|--|
| No. | Score | Query Match | Length | DB | ID | Description | |
| 1 | 1682 | 100.0 | 314 | 9 | US-09-970-989-15 | Sequence 15, Appl | |
| 2 | 1682 | 100.0 | 314 | 15 | US-10-667-494-15 | Sequence 15, Appl | |
| 3 | 1682 | 100.0 | 314 | 15 | US-10-667-462-15 | Sequence 15, Appl | |
| 4 | 1682 | 100.0 | 314 | 15 | US-10-667-464-15 | Sequence 15, Appl | |
| 5 | 1682 | 100.0 | 376 | 9 | US-09-970-989-13 | Sequence 13, Appl | |
| 6 | 1682 | 100.0 | 376 | 11 | US-09-833-245-1647 | Sequence 1647, Ap | |
| 7 | 1682 | 100.0 | 376 | 15 | US-10-296-606-9 | Sequence 9, Appli | |
| 8 | 1682 | 100.0 | 376 | 15 | US-10-667-494-13 | Sequence 13, Appl | |
| 9 | 1682 | 100.0 | 376 | 15 | US-10-667-462-13 | Sequence 13, Appl | |
| 10 | 1682 | 100.0 | 376 | 15 | US-10-667-464-13 | Sequence 13, Appl | |
| 11 | 1678 | 99.8 | 376 | 9 | US-09-798-029-6 | Sequence 6, Appli | |
| 12 | 1678 | 99.8 | 376 | 16 | US-10-737-450-36 | Sequence 36, Appl | |
| 13 | 1678 | 99.8 | 376 | 17 | US-10-772-636-22 | Sequence 22, Appl | |
| 14 | 1585.5 | 94.3 | 368 | 10 | US-09-946-374-297 | Sequence 297, App | |
| 15 | 1585.5 | 94.3 | 368 | 13 | US-10-052-586-338 | Sequence 338, App | |
| 16 | 1585.5 | 94.3 | 368 | 14 | US-10-174-590-338 | Sequence 338, App | |
| 17 | 1585.5 | 94.3 | 368 | 14 | US-10-176-758-338 | Sequence 338, App | |
| 18 | 1585.5 | 94.3 | 368 | 14 | US-10-175-737-338 | Sequence 338, App | |
| 19 | 1585.5 | 94.3 | 368 | 14 | US-10-174-581-338 | Sequence 338, App | |
| 20 | 1585.5 | 94.3 | 368 | 14 | US-10-176-483-338 | Sequence 338, App | |
| 21 | 1585.5 | 94.3 | 368 | 14 | US-10-176-749-338 | Sequence 338, App | |
| 22 | 1585.5 | 94.3 | 368 | 14 | US-10-176-914-338 | Sequence 338, App | |
| 23 | 1585.5 | 94.3 | 368 | 14 | US-10-176-915-338 | Sequence 338, App | |
| 24 | 1585.5 | 94.3 | 368 | 14 | US-10-173-706-338 | Sequence 338, App | |
| 25 | 1585.5 | 94.3 | 368 | 14 | US-10-175-738-338 | Sequence 338, App | |
| 26 | 1585.5 | 94.3 | 368 | 14 | US-10-175-752-338 | Sequence 338, App | |
| 27 | 1585.5 | 94.3 | 368 | 14 | US-10-176-482-338 | Sequence 338, App | |
| 28 | 1585.5 | 94.3 | 368 | 14 | US-10-176-757-338 | Sequence 338, App | |
| 29 | 1585.5 | 94.3 | 368 | 14 | US-10-176-913-338 | Sequence 338, App | |
| 30 | 1585.5 | 94.3 | 368 | 14 | US-10-180-552-338 | Sequence 338, App | |
| 31 | 1585.5 | 94.3 | 368 | 14 | US-10-180-557-338 | Sequence 338, App | |
| 32 | 1585.5 | 94.3 | 368 | 14 | US-10-173-700-338 | Sequence 338, App | |
| 33 | 1585.5 | 94.3 | 368 | 14 | US-10-174-572-338 | Sequence 338, App | |
| 34 | 1585.5 | 94.3 | 368 | 14 | US-10-174-579-338 | Sequence 338, App | |
| 35 | 1585.5 | 94.3 | 368 | 14 | US-10-174-582-338 | Sequence 338, App | |
| 36 | 1585.5 | 94.3 | 368 | 14 | US-10-174-588-338 | Sequence 338, App | |
| 37 | 1585.5 | 94.3 | 368 | 14 | US-10-175-739-338 | Sequence 338, App | |
| 38 | 1585.5 | 94.3 | 368 | 14 | US-10-175-740-338 | Sequence 338, App | |
| 39 | 1585.5 | 94.3 | 368 | 14 | US-10-175-743-338 | Sequence 338, App | |
| 40 | 1585.5 | 94.3 | 368 | 14 | US-10-176-488-338 | Sequence 338, App | |
| 41 | 1585.5 | 94.3 | 368 | 14 | US-10-176-492-338 | Sequence 338, App | |
| 42 | 1585.5 | 94.3 | 368 | 14 | US-10-176-747-338 | Sequence 338, App | |
| 43 | 1585.5 | 94.3 | 368 | 14 | US-10-176-750-338 | Sequence 338, App | |
| 44 | 1585.5 | 94.3 | 368 | 14 | US-10-176-985-338 | Sequence 338, App | |
| 45 | 1585.5 | 94.3 | 368 | 14 | US-10-176-987-338 | Sequence 338, App | |

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OM protein - protein search, using sw model

Run on: June 14, 2005, 16:16:02 ; Search time 39 Seconds
(without alignments)
774.668 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLLEWWSCTECTLFSTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| | | Match | Length | DB | | |
| 1 | 541 | 32.2 | 376 | 2 | D96550 | hypothetical prote |
| 2 | 510 | 30.3 | 377 | 2 | S60478 | probable 1-acyl-sn |
| 3 | 496.5 | 29.5 | 374 | 2 | S52645 | probable 1-acyl-gl |
| 4 | 394.5 | 23.5 | 310 | 2 | T06755 | probable glycerol- |
| 5 | 389.5 | 23.2 | 311 | 2 | T07936 | probable glycerol- |
| 6 | 346 | 20.6 | 393 | 2 | B96780 | hypothetical prote |
| 7 | 292 | 17.4 | 350 | 2 | T40466 | probable acetyltra |
| 8 | 279 | 16.6 | 397 | 2 | S45900 | probable membrane |
| 9 | 221.5 | 13.2 | 396 | 2 | S54641 | probable membrane |
| 10 | 215 | 12.8 | 344 | 2 | T31913 | hypothetical prote |
| 11 | 208.5 | 12.4 | 918 | 2 | T34057 | hypothetical prote |
| 12 | 196.5 | 11.7 | 523 | 2 | T25998 | hypothetical prote |
| 13 | 191 | 11.4 | 439 | 2 | T22689 | hypothetical prote |
| 14 | 170 | 10.1 | 363 | 2 | T20608 | hypothetical prote |

| | | | | | | |
|----|-------|-----|------|---|--------|--------------------|
| 15 | 161 | 9.6 | 304 | 2 | B83541 | probable polynucle |
| 16 | 152 | 9.0 | 295 | 2 | B83587 | probable polynucle |
| 17 | 140.5 | 8.4 | 310 | 2 | S40808 | polynucleotide ade |
| 18 | 140.5 | 8.4 | 310 | 2 | G86073 | probable endonucle |
| 19 | 140.5 | 8.4 | 310 | 2 | A91227 | probable endonucle |
| 20 | 133 | 7.9 | 294 | 2 | D82371 | probable polynucle |
| 21 | 129 | 7.7 | 391 | 2 | T15366 | hypothetical prote |
| 22 | 126 | 7.5 | 279 | 2 | T50125 | probable 1-acylgly |
| 23 | 126 | 7.5 | 302 | 2 | AI0950 | probable acyltrans |
| 24 | 114.5 | 6.8 | 247 | 2 | G72223 | hypothetical prote |
| 25 | 112 | 6.7 | 303 | 2 | A48600 | probable sn2-acylg |
| 26 | 102.5 | 6.1 | 936 | 2 | T26521 | hypothetical prote |
| 27 | 101.5 | 6.0 | 142 | 2 | T29793 | hypothetical prote |
| 28 | 96.5 | 5.7 | 257 | 2 | A83645 | probable acyltrans |
| 29 | 91.5 | 5.4 | 955 | 2 | F84972 | valine-tRNA ligase |
| 30 | 88 | 5.2 | 247 | 2 | A81957 | 1-acylglycerol-3-p |
| 31 | 87 | 5.2 | 288 | 2 | H95940 | probable xanthine |
| 32 | 86.5 | 5.1 | 301 | 2 | E82440 | hypothetical prote |
| 33 | 86 | 5.1 | 247 | 2 | G81013 | 1-acyl-sn-glycerol |
| 34 | 86 | 5.1 | 358 | 2 | C86291 | hypothetical prote |
| 35 | 86 | 5.1 | 451 | 2 | F75131 | hypothetical prote |
| 36 | 86 | 5.1 | 591 | 2 | F69837 | asparagine synthas |
| 37 | 86 | 5.1 | 956 | 2 | B71250 | valine-tRNA ligase |
| 38 | 85.5 | 5.1 | 531 | 2 | T11596 | hypothetical prote |
| 39 | 85.5 | 5.1 | 699 | 2 | C97176 | cation transport P |
| 40 | 84.5 | 5.0 | 283 | 2 | F90681 | taurine dioxygenas |
| 41 | 84.5 | 5.0 | 283 | 2 | B85532 | taurine dioxygenas |
| 42 | 84.5 | 5.0 | 416 | 2 | B88493 | protein F57B9.5 [i |
| 43 | 84 | 5.0 | 752 | 2 | G69457 | ribonucleoside-dip |
| 44 | 83.5 | 5.0 | 608 | 2 | H90530 | conserved hypothet |
| 45 | 83.5 | 5.0 | 1322 | 2 | T15689 | hypothetical prote |

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OM protein - protein search, using sw model

Run on: June 14, 2005, 16:19:22 ; Search time 123 Seconds
(without alignments)
1307.259 Million cell updates/sec

Title: US-10-667-462-15
Perfect score: 1682
Sequence: 1 MLEWWSCTECTLFTDQATV.....GVTEIEKGSSYGNQEFKKKE 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|--------------|---------------------|
| 1 | 1682 | 100.0 | 376 | 1 PLCC_HUMAN | Q9nrz7 homo sapien |
| 2 | 1662 | 98.8 | 392 | 2 Q6ZUC6 | Q6zuc6 homo sapien |
| 3 | 1632 | 97.0 | 307 | 2 Q8N3Q7 | Q8n3q7 homo sapien |
| 4 | 1598 | 95.0 | 376 | 2 Q7TT39 | Q7tt39 mus musculu |
| 5 | 1598 | 95.0 | 376 | 2 Q9D517 | Q9d517 m mus muscu |
| 6 | 1589 | 94.5 | 314 | 2 Q8BST2 | Q8bst2 mus musculu |
| 7 | 1585.5 | 94.3 | 368 | 2 Q6UWP6 | Q6uwp6 homo sapien |
| 8 | 1432 | 85.1 | 376 | 2 Q66J57 | Q66j57 xenopus lae |
| 9 | 1428 | 84.9 | 376 | 2 Q66IJ5 | Q66ij5 xenopus tro |
| 10 | 1420 | 84.4 | 376 | 2 Q7ZYI1 | Q7zyi1 xenopus lae |
| 11 | 1286.5 | 76.5 | 377 | 2 Q7ZWC9 | Q7zwc9 brachydanio |
| 12 | 1138 | 67.7 | 377 | 2 Q6IRA0 | Q6ira0 xenopus lae |
| 13 | 1094 | 65.0 | 378 | 1 PLCD_HUMAN | Q9nrz5 h 1-acyl-sn |
| 14 | 1085 | 64.5 | 378 | 2 Q8K4X7 | Q8k4x7 m lysosphosp |
| 15 | 1084 | 64.4 | 377 | 2 Q6PGY2 | Q6pgy2 brachydanio |
| 16 | 1084 | 64.4 | 378 | 1 PLCD_RAT | Q924s1 rattus norv |

| | | | | | | | |
|----|-------|------|-----|---|------------|--------|-------------|
| 17 | 645 | 38.3 | 386 | 2 | Q9VV51 | Q9vv51 | drosophila |
| 18 | 644.5 | 38.3 | 442 | 2 | Q7QIX2 | Q7qix2 | anopheles g |
| 19 | 622 | 37.0 | 380 | 2 | Q9VV49 | Q9vv49 | drosophila |
| 20 | 541 | 32.2 | 376 | 2 | Q9SYC8 | Q9syc8 | arabidopsis |
| 21 | 521.5 | 31.0 | 391 | 2 | Q6IYW1 | Q6iwy1 | brassica ol |
| 22 | 517.5 | 30.8 | 390 | 2 | Q9XFW4 | Q9xfw4 | brassica na |
| 23 | 513.5 | 30.5 | 389 | 2 | Q8LG50 | Q8lg50 | arabidopsis |
| 24 | 510 | 30.3 | 377 | 2 | Q40119 | Q40119 | limnanthes |
| 25 | 496.5 | 29.5 | 374 | 2 | Q41745 | Q41745 | zea mays (m |
| 26 | 485 | 28.8 | 306 | 2 | Q9SDN3 | Q9sdn3 | prunus dulc |
| 27 | 394.5 | 23.5 | 310 | 2 | Q9SVX9 | Q9svx9 | arabidopsis |
| 28 | 392 | 23.3 | 237 | 2 | Q7X9L2 | Q7x9l2 | triticum ae |
| 29 | 389.5 | 23.2 | 311 | 2 | Q39317 | Q39317 | brassica na |
| 30 | 358 | 21.3 | 375 | 2 | Q9LHN4 | Q9lhn4 | arabidopsis |
| 31 | 350 | 20.8 | 378 | 2 | Q8L4Y2 | Q8l4y2 | arabidopsis |
| 32 | 346 | 20.6 | 373 | 2 | Q9SSH0 | Q9ssh0 | arabidopsis |
| 33 | 346 | 20.6 | 393 | 2 | Q9C9P8 | Q9c9p8 | arabidopsis |
| 34 | 292 | 17.4 | 350 | 2 | O94361 | O94361 | schizosacch |
| 35 | 279.5 | 16.6 | 414 | 2 | Q6UWP7 | Q6uwp7 | homo sapien |
| 36 | 279 | 16.6 | 397 | 1 | YB42_YEAST | P38226 | saccharomyc |
| 37 | 267.5 | 15.9 | 428 | 2 | Q7S0V1 | Q7s0v1 | neurospora |
| 38 | 252 | 15.0 | 388 | 2 | Q6NYV8 | Q6nyv8 | brachydanio |
| 39 | 248.5 | 14.8 | 409 | 2 | Q6C336 | Q6c336 | yarrowia li |
| 40 | 243.5 | 14.5 | 411 | 2 | Q75CU2 | Q75cu2 | ashbya goss |
| 41 | 238.5 | 14.2 | 397 | 2 | Q6FQP4 | Q6fqp4 | candida gla |
| 42 | 237.5 | 14.1 | 404 | 2 | Q6CW53 | Q6cw53 | kluyveromyc |
| 43 | 228 | 13.6 | 356 | 2 | Q6NUM7 | Q6num7 | homo sapien |
| 44 | 228 | 13.6 | 364 | 1 | PLCE_HUMAN | Q9nuq2 | homo sapien |
| 45 | 221.5 | 13.2 | 396 | 1 | YD18_YEAST | Q12185 | saccharomyc |